



results of BLAST

BLASTN 2.2.2 [Dec-14-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1015614256-23862-18740

Query=

(20 letters)

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions

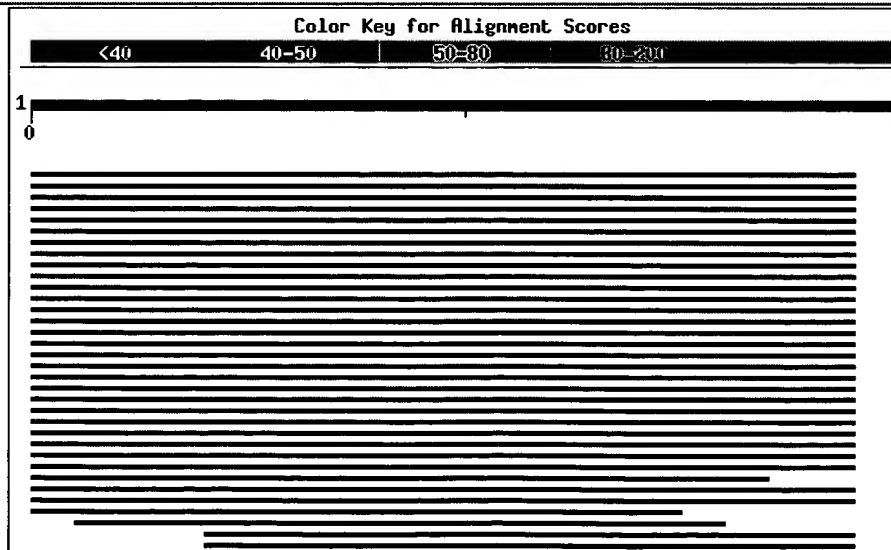
10,685,586 sequences; 5,029,563,727 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 34 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

							Score (bits)	E Value
gi	18173255	gb	BM348643.1	BM348643	MEST294-C01.T3	ISUM5-RN ...	40	0.012
gi	18171102	gb	BM340942.1	BM340942	MEST328-A09.T3	ISUM5-RN ...	40	0.012
gi	18169253	gb	BM339093.1	BM339093	MEST236-F10.T3	ISUM5-RN ...	40	0.012
gi	18167158	gb	BM336997.1	BM336997	MEST201-H09.T3	ISUM5-RN ...	40	0.012
gi	18164243	gb	BM334082.1	BM334082	MEST132-C11.T3	ISUM5-RN ...	40	0.012

gi	17931830	gb	BM268790.1	BM268790	MEST400-E11.univ ISUM5-R...	40	0.012
gi	17930245	gb	BM267205.1	BM267205	MEST391-F01.T3 ISUM5-RN ...	40	0.012
gi	17930061	gb	BM267021.1	BM267021	MEST389-B08.T3 ISUM5-RN ...	40	0.012
gi	16926819	gb	BM079887.1	BM079887	MEST101-A03.T3 ISUM4-TN ...	40	0.012
gi	16926507	gb	BM079570.1	BM079570	MEST96-D10.T3 ISUM4-TN Z...	40	0.012
gi	16925569	gb	BM078637.1	BM078637	MEST122-D04.T3 ISUM4-TN ...	40	0.012
gi	16922583	gb	BM075638.1	BM075638	MEST358-C04.T3 ISUM5-RN ...	40	0.012
gi	16919855	gb	BM074388.1	BM074388	MEST85-E10.T3 ISUM4-TN Z...	40	0.012
gi	13126315	gb	BG316885.1	BG316885	947027G05.x1 947 - 2 wee...	40	0.012
gi	7119143	gb	AW497500.1	AW497500	660052H09.x1 660 - Mixed ...	40	0.012
gi	6056718	gb	AW091123.1	AW091123	614091A08.x1 614 - root c...	40	0.012
gi	6022239	gb	AW067167.1	AW067167	683016F05.x1 683 - 14 day...	40	0.012
gi	5847127	gb	AW000206.1	AW000206	614009A12.y1 614 - root c...	40	0.012
gi	5791446	gb	AI978238.1	AI978238	614042B09.x2 614 - root c...	40	0.012
gi	5740565	gb	AI948255.1	AI948255	603039C05.x1 603 - stress...	40	0.012
gi	5714248	gb	AI944233.1	AI944233	614039C05.x1 614 - root c...	40	0.012
gi	5607926	gb	AI901593.1	AI901593	618007E09.x1 618 - Inbred...	40	0.012
gi	5525452	gb	AI861345.1	AI861345	614012F08.x1 614 - root c...	40	0.012
gi	5499176	gb	AI855043.1	AI855043	606074C08.x1 606 - Ear ti...	40	0.012
gi	5343195	gb	AI795380.1	AI795380	614009A12.x2 614 - root c...	40	0.012
gi	5018372	gb	AI714565.1	AI714565	605059E11.x1 605 - Endosp...	40	0.012
gi	4967137	gb	AI691859.1	AI691859	606011C12.x1 606 - Ear ti...	40	0.012
gi	18163119	gb	BM332958.1	BM332958	MEST182-A04.T3 ISUM5-RN ...	36	0.19
gi	18172136	gb	BM347524.1	BM347524	MEST278-G04.T3 ISUM5-RN ...	32	2.9
gi	18169928	gb	BM339768.1	BM339768	MEST312-C12.T3 ISUM5-RN ...	32	2.9
gi	18166927	gb	BM336766.1	BM336766	MEST198-F01.T3 ISUM5-RN ...	32	2.9
gi	16083856	gb	BI876585.1	BI876585	fl74b04.y1 Sugano Kawaka...	32	2.9
gi	6950713	gb	AW422781.1	AW422781	fi47f07.y1 Sugano Kawakam...	32	2.9
gi	3675335	gb	AI147653.1	AI147653	qb27e01.x1 Soares_pregnan...	32	2.9

Alignments

>gi|18173255|gb|BM348643.1|BM348643 MEST294-C01.T3 ISUM5-RN Zea mays cDNA clone MEST29
Length = 548

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
|||||||
Sbjct: 142 gttttccgtctagcctcggt 123

>gi|18171102|gb|BM340942.1|BM340942 MEST328-A09.T3 ISUM5-RN Zea mays cDNA clone MEST32
Length = 232

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
|||||||
Sbjct: 217 gttttccgtctagcctcggt 198

>gi|18169253|gb|BM339093.1|BM339093 MEST236-F10.T3 ISUM5-RN Zea mays cDNA clone MEST23
Length = 650

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20

|||||
 Sbjct: 215 gttttccgtctagcctcggt 196

>gi|18167158|gb|BM336997.1|BM336997 MEST201-H09.T3 ISUM5-RN Zea mays cDNA clone MEST20
 Length = 752

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 215 gttttccgtctagcctcggt 196

>gi|18164243|gb|BM334082.1|BM334082 MEST132-C11.T3 ISUM5-RN Zea mays cDNA clone MEST13
 Length = 594

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 216 gttttccgtctagcctcggt 197

>gi|17931830|gb|BM268790.1|BM268790 MEST400-E11.univ ISUM5-RN Zea mays cDNA clone MEST
 Length = 745

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 215 gttttccgtctagcctcggt 196

>gi|17930245|gb|BM267205.1|BM267205 MEST391-F01.T3 ISUM5-RN Zea mays cDNA clone MEST39
 Length = 555

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 217 gttttccgtctagcctcggt 198

>gi|17930061|gb|BM267021.1|BM267021 MEST389-B08.T3 ISUM5-RN Zea mays cDNA clone MEST38
 Length = 746

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 215 gttttccgtctagcctcggt 196

>gi|16926819|gb|BM079887.1|BM079887 MEST101-A03.T3 ISUM4-TN Zea mays cDNA clone MEST10
 Length = 530

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
|||||||
Sbjct: 142 gttttccgtctagcctcggt 123

>gi|16926507|gb|BM079570.1|BM079570 MEST96-D10.T3 ISUM4-TN Zea mays cDNA clone MEST96-
Length = 697

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 1 gttttccgtctagcctcggt 20
|||||||
Sbjct: 578 gttttccgtctagcctcggt 597

>gi|16925569|gb|BM078637.1|BM078637 MEST122-D04.T3 ISUM4-TN Zea mays cDNA clone MEST12
Length = 626

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
|||||||
Sbjct: 145 gttttccgtctagcctcggt 126

>gi|16922583|gb|BM075638.1|BM075638 MEST358-C04.T3 ISUM5-RN Zea mays cDNA clone MEST35
Length = 512

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
|||||||
Sbjct: 215 gttttccgtctagcctcggt 196

>gi|16919855|gb|BM074388.1|BM074388 MEST85-E10.T3 ISUM4-TN Zea mays cDNA clone MEST85-
Length = 670

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
|||||||
Sbjct: 151 gttttccgtctagcctcggt 132

>gi|13126315|gb|BG316885.1|BG316885 947027G05.x1 947 - 2 week shoot from Barkan lab Ze
Length = 402

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 46 gttttccgtctagcctcggt 27

>gi|7119143|gb|AW497500.1|AW497500 660052H09.x1 660 - Mixed stages of anther and polle
 Length = 492

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 141 gttttccgtctagcctcggt 122

>gi|6056718|gb|AW091123.1|AW091123 614091A08.x1 614 - root cDNA library from Walbot La
 cDNA.
 Length = 561

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 87 gttttccgtctagcctcggt 68

>gi|6022239|gb|AW067167.1|AW067167 683016F05.x1 683 - 14 day immature embryo from Hake
 mays cDNA.
 Length = 583

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 145 gttttccgtctagcctcggt 126

>gi|5847127|gb|AW000206.1|AW000206 614009A12.y1 614 - root cDNA library from Walbot La
 Length = 554

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Plus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 416 gttttccgtctagcctcggt 435

>gi|5791446|gb|AI978238.1|AI978238 614042B09.x2 614 - root cDNA library from Walbot La
 cDNA.
 Length = 411

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20

|||||
 Sbjct: 94 gttttccgtctagcctcggt 75

>gi|5740565|gb|AI948255.1|AI948255 603039C05.x1 603 - stressed root cDNA library from
 Zea mays cDNA.
 Length = 528

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 124 gttttccgtctagcctcggt 105

>gi|5714248|gb|AI944233.1|AI944233 614039C05.x1 614 - root cDNA library from Walbot La
 cDNA.
 Length = 416

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 43 gttttccgtctagcctcggt 24

>gi|5607926|gb|AI901593.1|AI901593 618007E09.x1 618 - Inbred Tassel cDNA Library Zea m
 Length = 409

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 98 gttttccgtctagcctcggt 79

>gi|5525452|gb|AI861345.1|AI861345 614012F08.x1 614 - root cDNA library from Walbot La
 Length = 627

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 103 gttttccgtctagcctcggt 84

>gi|5499176|gb|AI855043.1|AI855043 606074C08.x1 606 - Ear tissue cDNA library from Sch
 mays cDNA.
 Length = 605

Score = 40.1 bits (20), Expect = 0.012
 Identities = 20/20 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 145 gttttccgtctagcctcggt 126

>gi|5343195|gb|AI795380.1|AI795380 614009A12.x2 614 - root cDNA library from Walbot La
Length = 554

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 1 gttttccgtctagcctcggt 20
 |||||
Sbjct: 416 gttttccgtctagcctcggt 435

>gi|5018372|gb|AI714565.1|AI714565 605059E11.x1 605 - Endosperm cDNA library from Schm
mays cDNA.
Length = 581

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
Sbjct: 85 gttttccgtctagcctcggt 66

>gi|4967137|gb|AI691859.1|AI691859 606011C12.x1 606 - Ear tissue cDNA library from Sch
mays cDNA.
Length = 595

Score = 40.1 bits (20), Expect = 0.012
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
Sbjct: 136 gttttccgtctagcctcggt 117

>gi|18163119|gb|BM332958.1|BM332958 MEST182-A04.T3 ISUM5-RN Zea mays cDNA clone MEST18
Length = 513

Score = 36.2 bits (18), Expect = 0.19
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcg 18
 |||||
Sbjct: 213 gttttccgtctagcctcg 196

>gi|18172136|gb|BM347524.1|BM347524 MEST278-G04.T3 ISUM5-RN Zea mays cDNA clone MEST27
Length = 609

Score = 32.2 bits (16), Expect = 2.9
Identities = 19/20 (95%)
Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
Sbjct: 214 gttttccgtctagcatcggt 195

>gi|18169928|gb|BM339768.1|BM339768 MEST312-C12.T3 ISUM5-RN Zea mays cDNA clone MEST31
Length = 645

Score = 32.2 bits (16), Expect = 2.9
 Identities = 19/20 (95%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcctcggt 20
 |||||
 Sbjct: 214 gttttccgtctagcatcggt 195

>gi|18166927|gb|BM336766.1|BM336766 MEST198-F01.T3 ISUM5-RN Zea mays cDNA clone MEST19
 Length = 533

Score = 32.2 bits (16), Expect = 2.9
 Identities = 16/16 (100%)
 Strand = Plus / Minus

Query: 1 gttttccgtctagcct 16
 |||||
 Sbjct: 209 gttttccgtctagcct 194

>gi|16083856|gb|BI876585.1|BI876585 fl74b04.y1 Sugano Kawakami zebrafish DRA Danio rer
 3819582 5' similar to TR:Q9Y6X8 Q9Y6X8 KIAA0854
 PROTEIN. ;.
 Length = 628

Score = 32.2 bits (16), Expect = 2.9
 Identities = 16/16 (100%)
 Strand = Plus / Plus

Query: 5 tccgtctagcctcggt 20
 |||||
 Sbjct: 7 tccgtctagcctcggt 22

>gi|6950713|gb|AW422781.1|AW422781 fi47f07.y1 Sugano Kawakami zebrafish DRA Danio reri
 2640805 5' similar to TR:Q60566 Q60566 VDX ;.
 Length = 622

Score = 32.2 bits (16), Expect = 2.9
 Identities = 16/16 (100%)
 Strand = Plus / Plus

Query: 5 tccgtctagcctcggt 20
 |||||
 Sbjct: 1 tccgtctagcctcggt 16

>gi|3675335|gb|AI147653.1|AI147653 qb27e01.x1 Soares_pregnant_uterus_NbHPU Homo sapien
 IMAGE:1697496 3'.
 Length = 268

Score = 32.2 bits (16), Expect = 2.9
 Identities = 16/16 (100%)
 Strand = Plus / Plus

Query: 2 ttttccgtctagcctc 17
 |||||
 Sbjct: 193 ttttccgtctagcctc 208

Database: Database of GenBank+EMBL+DDBJ sequences from EST Divisions

Posted date: Mar 6, 2002 2:52 AM

Number of letters in database: 734,596,431

Number of sequences in database: 10,685,586

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 5932
Number of Sequences: 10685586
Number of extensions: 5932
Number of successful extensions: 5911
Number of sequences better than 10.0: 34
length of query: 20
length of database: 5,029,563,727
effective HSP length: 17
effective length of query: 3
effective length of database: 4,847,908,765
effective search space: 14543726295
effective search space used: 14543726295
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 16 (32.2 bits)